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By

Name of person signing: Jocelyn L. Lee

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application for:

Charles A. NICOLETTE

Serial No.: 09/812,238

Filing Date: March 19, 2001

For: THERAPEUTIC ANTI-MELANOMA
COMPOUNDS

Examiner: Not Yet Assigned

Group Art Unit: Not Yet Assigned

Commissioner for Patents
Washington, D.C. 20231

SUBMISSION OF SEQUENCE LISTING

Dear Sir:

The Applicants hereby declare that the content of the computer-readable form of the Sequence Listing is identical to the written Listing concurrently filed herewith.

DATE: December 18, 2001

Respectfully submitted,

By:

Antoinette F. Konski

Registration No.: 34,202

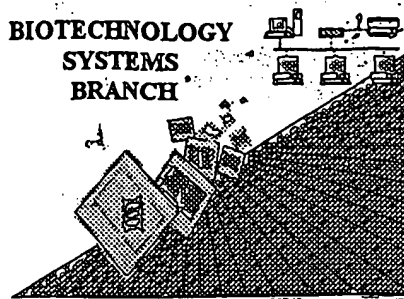
Michele Todd Wasmuth

Registration No.: 43,239

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Three Embarcadero Center, Suite 1800
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Telephone: (650) 849-4936
Telefax: (650) 849-4800

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/812,238
Source: OIP
Date Processed by STIC: 8/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

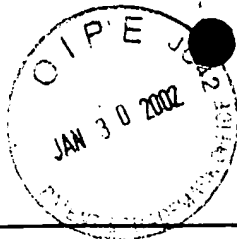
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>



Raw Sequence Listing Error Summary

ERROR DETECTED

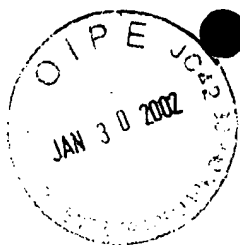
SUGGESTED CORRECTION

SERIAL NUMBER: 09/812,238

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/812,238

DATE: 08/02/2001
TIME: 17:34:41

Input Set : A:\sequence.txt
Output Set: N:\CRF3\08022001\I812238.raw

Does Not Comply
Corrected Diskette Needed!

3 <110> APPLICANT: Nicolette, Charles
5 <120> TITLE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
8 <130> FILE REFERENCE: 126881309400
10 <140> CURRENT APPLICATION NUMBER: US/09/812,238
11 <141> CURRENT FILING DATE: 2001-03-19
13 <160> NUMBER OF SEQ ID NOS: 19
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0

pg 1-2

ERRORED SEQUENCES

298 <210> SEQ ID NO: 4	
299 <211> LENGTH: 27	
300 <212> TYPE: DNA	
301 <213> ORGANISM: Homo sapiens	
303 <400> SEQUENCE: 4	
E--> 304 wsnttygayc argtnccntt ywsngtn	27
315 <210> SEQ ID NO: 6	
316 <211> LENGTH: 27	
317 <212> TYPE: DNA	
318 <213> ORGANISM: Homo sapiens	
320 <400> SEQUENCE: 6	
E--> 321 ttywsngayc argtnccntt ywsngtn	27
332 <210> SEQ ID NO: 8	
333 <211> LENGTH: 27	
334 <212> TYPE: DNA	
335 <213> ORGANISM: Homo sapiens	
337 <400> SEQUENCE: 8	
E--> 338 gngtngayc argtnccntt ywsngtn	27
349 <210> SEQ ID NO: 10	
350 <211> LENGTH: 27	
351 <212> TYPE: DNA	
352 <213> ORGANISM: Homo sapiens	
354 <400> SEQUENCE: 10	
E--> 355 atgacngayc argtnccntt ywsngtn	27
366 <210> SEQ ID NO: 12	
367 <211> LENGTH: 27	
368 <212> TYPE: DNA	
369 <213> ORGANISM: Homo sapiens	
371 <400> SEQUENCE: 12	
E--> 372 gcnathgayc argtnccntt ywsngtn	27
383 <210> SEQ ID NO: 14	
384 <211> LENGTH: 27	
385 <212> TYPE: DNA	
386 <213> ORGANISM: Homo sapiens	
388 <400> SEQUENCE: 14	
E--> 389 ytnathgayc argtnccntt ywsngtn	27

see item 9 on Error Summary Sheet

item 9

item 9

item 9

item 9

item 9

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/812,238

DATE: 08/02/2001

TIME: 17:34:41

Input Set : A:\sequence.txt

Output Set: N:\CRF3\08022001\I812238.raw

400 <210> SEQ ID NO: 16

401 <211> LENGTH: 27

402 <212> TYPE: DNA

403 <213> ORGANISM: Homo sapiens

405 <400> SEQUENCE: 16

E--> 406 atggtn gayc argtnccntt ywsngtn *dem 9*

27

417 <210> SEQ ID NO: 18

418 <211> LENGTH: 27

419 <212> TYPE: DNA

420 <213> ORGANISM: Homo sapiens

422 <400> SEQUENCE: 18

E--> 423 caygtngayc argtnccntt ywsngtn *dem 9*

27

425 <210> SEQ ID NO: 19

426 <211> LENGTH: 9

427 <212> TYPE: PRT

428 <213> ORGANISM: Homo sapiens

430 <400> SEQUENCE: 19

431 Ile Thr Asp Gln Val Pro Phe Ser Val

432 1 5

E--> 433 ①

delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/812,238

DATE: 08/02/2001

TIME: 17:34:42

Input Set : A:\sequence.txt

Output Set: N:\CRF3\08022001\I812238.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:304 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:321 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:338 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:372 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:389 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:406 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:423 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:433 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19